

Amendments

In the Specification:

Please substitute the following paragraphs/sections for the pending paragraphs/sections.

Please replace the paragraph beginning on page 98, line 19, with the following:

B¹

As one of ordinary skill would appreciate, due to the possibilities of sequencing errors, as well as the variability of cleavage sites for leaders in different known proteins, the predicted METH1 polypeptide encoded by the deposited cDNA comprises about 950 amino acids, but may be anywhere in the range of 910-990 amino acids; and the predicted leader sequence of this protein is about 28 amino acids, but may be anywhere in the range of about 18 to about 38 amino acids. An alternative predicted METH1 polypeptide is shown in SEQ ID NO:126, encoded by SEQ ID NO:125, and comprises an additional 18 amino acid residues on the N-terminus. Also, the predicted METH2 polypeptide comprises about 890 amino acids, but may be anywhere in the range of 850 to about 930 amino acids; and the predicted leader sequence of this protein is about 23 amino acids, but may be anywhere in the range of about 13 to about 33 amino acids.

Please replace the paragraph beginning on page 216, line 21, with the following:

B²

Deletion mutants of METH1 may also be made which comprise all or part of the additional sequence described in SEQ ID NO:126. For example, exemplary deletion